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SEQUENCE LISTING

<110> CHERESH, David A.
ELICEIRI, Brian
SCHWARTZBERG, Pamela L.

<120> METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF
ANGIOGENESIS USING TYROSINE KINASE SRC

<130> TSRI 651.1

<140> US 09/701,500
<141> 2000-11-29

<150> PCT/US99/11780
<151> 1999-05-28

<150> US 60/087,220
<151> 1998-05-29

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<170> PatentIn Ver. 2.0

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 <213> Chicken

<220>

<221> gene
 <222> (1)..(1759)
 <223> chicken c-SRC cDNA

<220>

<221> CDS
 <222> (112)..(1710)

<400> 2
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 cctcgctac cactgtggcc aggcggtagc tgggacgtgc agcccaccac c atg ggg 117
 Met Gly
 1
 agc agc aag agc aag ccc aag gac ccc agc cag cgc cgg cgc agc ctg 165
 Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg Arg Arg Ser Leu
 5 10 15
 gag cca ccc gac agc acc cac cac ggg gga ttc cca gcc tcg cag acc 213
 Glu Pro Pro Asp Ser Thr His His Gly Gly Phe Pro Ala Ser Gln Thr
 20 25 30
 ccc aac aag aca gca gcc ccc gac acg cac cgc acc ccc agc cgc tcc 261
 Pro Asn Lys Thr Ala Ala Pro Asp Thr His Arg Thr Pro Ser Arg Ser
 35 40 45 50
 ttt ggg acc gtg gcc acc gag ccc aag ctc ttc ggg ggc ttc aac act 309
 Phe Gly Thr Val Ala Thr Glu Pro Lys Leu Phe Gly Gly Phe Asn Thr
 55 60 65
 tct gac acc gtt acg tcg ccg cag cgt gcc ggg gca ctg gct ggc ggc 357
 Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly Ala Leu Ala Gly Gly
 70 75 80
 gtc acc act ttc gtg gct ctc tac gac tac gag tcc cgg act gaa acg 405
 Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu Ser Arg Thr Glu Thr
 85 90 95
 gac ttg tcc ttc aag aaa gga gaa cgc ctg cag att gtc aac aac acg 453
 Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln Ile Val Asn Asn Thr
 100 105 110
 gaa ggt gac tgg tgg ctg gct cat tcc ctc act aca gga cag acg ggc 501
 Glu Gly Asp Trp Trp Leu Ala His Ser Leu Thr Thr Gly Gln Thr Gly
 115 120 125 130

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tac atc ccc agt aac tat gtc gcg ccc tca gac tcc atc cag gct gaa	549
Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp Ser Ile Gln Ala Glu	
135 140 145	
gag tgg tac ttt ggg aag atc act cgt cgg gag tcc gag cgg ctg ctg	597
Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser Glu Arg Leu Leu	
150 155 160	
ctc aac ccc gaa aac ccc cgg gga acc ttc ttg gtc cgg gag agc gag	645
Leu Asn Pro Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu Ser Glu	
165 170 175	
acg aca aaa ggt gcc tat tgc ctc tcc gtt tct gac ttt gac aac gcc	693
Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp Phe Asp Asn Ala	
180 185 190	
aag ggg ctc aat gtg aag cac tac aag atc cgc aag ctg gac agc ggc	741
Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys Leu Asp Ser Gly	
195 200 205 210	
ggc ttc tac atc acc tca cgc aca cag ttc agc agc ctg cag cag ctg	789
Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Ser Ser Leu Gln Gln Leu	
215 220 225	
gtg gcc tac tac tcc aaa cat gct gat ggc ttg tgc cac cgc ctg acc	837
Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys His Arg Leu Thr	
230 235 240	
aac gtc tgc ccc acg tcc aag ccc cag acc cag gga ctc gcc aag gac	885
Asn Val Cys Pro Thr Ser Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp	
245 250 255	
gcg tgg gaa atc ccc cgg gag tcg ctg cgg ctg gag gtg aag ctg ggg	933
Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly	
260 265 270	
cag ggc tgc ttt gga gag gtc tgg atg ggg acc tgg aac ggc acc acc	981
Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr	
275 280 285 290	
aga gtg gcc ata aag act ctg aag ccc ggc acc atg tcc ccg gag gcc	1029
Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Glu Ala	
295 300 305	
ttc ctg cag gaa gcc caa gtg atg aag aag ctc cgg cat gag aag ctg	1077
Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu Arg His Glu Lys Leu	
310 315 320	
gtt cag ctg tac gca gtg gtg tcg gaa gag ccc atc tac atc gtc act	1125
Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr	
325 330 335	
gag tac atg agc aag ggg agc ctc ctg gat ttc ctg aag gga gag atg	1173
Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly Glu Met	
340 345 350	
ggc aag tac ctg cgg ctg cca cag ctc gtc gat atg gct gct cag att	1221
Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile	
355 360 365 370	

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gca tcc ggc atg gcc tat gtg gag agg atg aac tac gtg cac cga gac 1269
 Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His Arg Asp
 375 380 385

ctg cgg gcg gcc aac atc ctg gtg ggg gag aac ctg gtg tgc aag gtg 1317
 Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Val
 390 395 400

gct gac ttt ggg ctg gca cgc ctc atc gag gac aac gag tac aca gca 1365
 Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala
 405 410 415

cgg caa ggt gcc aag ttc ccc atc aag tgg aca gcc ccc gag gca gcc 1413
 Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala
 420 425 430

ctc tat ggc cgg ttc acc atc aag tcg gat gtc tgg tcc ttc ggc atc 1461
 Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile
 435 440 445 450

ctg ctg act gag ctg acc acc aag ggc cgg gtg cca tac cca ggg atg 1509
 Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro Gly Met
 455 460 465

gtc aac agg gag gtg ctg gac cag gtg gag agg ggc tac cgc atg ccc 1557
 Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg Gly Tyr Arg Met Pro
 470 475 480

tgc ccg ccc gag tgc ccc gag tcg ctg cat gac ctc atg tgc cag tgc 1605
 Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp Leu Met Cys Gln Cys
 485 490 495

tgg cgg agg gac cct gag gag cgg ccc act ttt gag tac ctg cag gcc 1653
 Trp Arg Arg Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ala
 500 505 510

ttc ctg gag gac tac ttc acc tcg aca gag ccc cag tac cag cct gga 1701
 Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro Gln Tyr Gln Pro Gly
 515 520 525 530

gag aac cta taggcctgga gctcctcctg gaccagaggc ctcgctgtgg ggtacaggg 1759
 Glu Asn Leu

<210> 3
 <211> 533
 <212> PRT
 <213> Chicken

<400> 3

Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg Arg Arg
 1 5 10 15

Ser Leu Glu Pro Pro Asp Ser Thr His His Gly Gly Phe Pro Ala Ser
 20 25 30

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Gln Thr Pro Asn Lys Thr Ala Ala Pro Asp Thr His Arg Thr Pro Ser
 35 40 45
 Arg Ser Phe Gly Thr Val Ala Thr Glu Pro Lys Leu Phe Gly Gly Phe
 50 55 60
 Asn Thr Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly Ala Leu Ala
 65 70 75 80
 Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu Ser Arg Thr
 85 90 95
 Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln Ile Val Asn
 100 105 110
 Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Thr Thr Gly Gln
 115 120 125
 Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp Ser Ile Gln
 130 135 140
 Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser Glu Arg
 145 150 155 160
 Leu Leu Leu Asn Pro Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu
 165 170 175
 Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp Phe Asp
 180 185 190
 Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys Leu Asp
 195 200 205
 Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Ser Ser Leu Gln
 210 215 220
 Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys His Arg
 225 230 235 240
 Leu Thr Asn Val Cys Pro Thr Ser Lys Pro Gln Thr Gln Gly Leu Ala
 245 250 255
 Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys
 260 265 270
 Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly
 275 280 285
 Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro
 290 295 300
 Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu Arg His Glu
 305 310 315 320
 Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile
 325 330 335

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Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly
 340 345 350
 Glu Met Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala
 355 360 365
 Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His
 370 375 380
 Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys
 385 390 395 400
 Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr
 405 410 415
 Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu
 420 425 430
 Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe
 435 440 445
 Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro
 450 455 460
 Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg Gly Tyr Arg
 465 470 475 480
 Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp Leu Met Cys
 485 490 495
 Gln Cys Trp Arg Arg Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu
 500 505 510
 Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro Gln Tyr Gln
 515 520 525
 Pro Gly Glu Asn Leu
 530

<210> 4
 <211> 2187
 <212> DNA
 <213> Homo sapiens

<220>
 <221> gene
 <222> (1)..(2187)
 <223> human c-SRC cDNA

<220>
 <221> CDS
 <222> (134)..(1483)

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 caagagagct ctaatggtac caagtgcacag gttggcttta ctgtgactcg gggacgccag 120
 agctcctgag aag atg tca gca ata cag gcc gcc tgg cca tcc ggt aca 169
 Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr
 1 5 10
 gaa tgt att gcc aag tac aac ttc cac ggc act gcc gag cag gac ctg 217
 Glu Cys Ile Ala Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu
 15 20 25
 ccc ttc tgc aaa gga gac gtg ctc acc att gtg gcc gtc acc aag gac 265
 Pro Phe Cys Lys Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp
 30 35 40
 ccc aac tgg tac aaa gcc aaa aac aag gtg ggc cgt gag ggc atc atc 313
 Pro Asn Trp Tyr Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile
 45 50 55 60
 cca gcc aac tac gtc cag aag cgg gag ggc gtg aag gcg ggt acc aaa 361
 Pro Ala Asn Tyr Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys
 65 70 75
 ctc agc ctc atg cct tgg ttc cac ggc aag atc aca cgg gag cag gct 409
 Leu Ser Leu Met Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala
 80 85 90
 gag cgg ctt ctg tac ccg ccg gag aca ggc ctg ttc ctg gtg cgg gag 457
 Glu Arg Leu Leu Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu
 95 100 105
 agc acc aac tac ccc gga gac tac acg ctg tgc gtg agc tgc gac ggc 505
 Ser Thr Asn Tyr Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly
 110 115 120
 aag gtg gag cac tac cgc atc atg tac cat gcc agc aag ctc agc atc 553
 Lys Val Glu His Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile
 125 130 135 140
 gac gag gag gtg tac ttt gag aac ctc atg cag ctg gtg gag cac tac 601
 Asp Glu Glu Val Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr
 145 150 155
 acc tca gac gca gat gga ctc tgt acg cgc ctc att aaa cca aag gtc 649
 Thr Ser Asp Ala Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val
 160 165 170
 atg gag ggc aca gtg gcg gcc cag gat gag ttc tac cgc agc ggc tgg 697
 Met Glu Gly Thr Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp
 175 180 185
 gcc ctg aac atg aag gag ctg aag ctg ctg cag acc atc ggg aag ggc 745
 Ala Leu Asn Met Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly
 190 195 200

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gag ttc gga gac gtg atg ctg ggc gat tac cga ggg aac aaa gtc gcc	793
Glu Phe Gly Asp Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala	
205 210 215 220	
gtc aag tgc att aag aac gac gcc act gcc cag gcc ttc ctg gct gaa	841
Val Lys Cys Ile Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu	
225 230 235	
gcc tca gtc atg acg caa ctg cgg cat agc aac ctg gtg cag ctc ctg	889
Ala Ser Val Met Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu	
240 245 250	
ggc gtg atc gtg gag gag aag ggc ggg ctc tac atc gtc act gag tac	937
Gly Val Ile Val Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr	
255 260 265	
atg gcc aag ggg agc ctt gtg gac tac ctg cgg tct agg ggt cgg tca	985
Met Ala Lys Gly Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser	
270 275 280	
gtg ctg ggc gga gac tgt ctc ctc aag ttc tcg cta gat gtc tgc gag	1033
Val Leu Gly Gly Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu	
285 290 295 300	
gcc atg gaa tac ctg gag ggc aac aat ttc gtg cat cga gac ctg gct	1081
Ala Met Glu Tyr Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala	
305 310 315	
gcc cgc aat gtg ctg gtg tct gag gac aac gtg gcc aag gtc agc gac	1129
Ala Arg Asn Val Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp	
320 325 330	
ttt ggt ctc acc aag gag gcg tcc agc acc cag gac acg ggc aag ctg	1177
Phe Gly Leu Thr Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu	
335 340 345	
cca gtc aag tgg aca gcc cct gag gcc ctg aga gag aag aaa ttc tcc	1225
Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser	
350 355 360	
act aag tct gac gtg tgg agt ttc gga atc ctt ctc tgg gaa atc tac	1273
Thr Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr	
365 370 375 380	
tcc ttt ggg cga gtg cct tat cca aga att ccc ctg aag gac gtc gtc	1321
Ser Phe Gly Arg Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val	
385 390 395	
cct cgg gtg gag aag ggc tac aag atg gat gcc ccc gac ggc tgc ccg	1369
Pro Arg Val Glu Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro	
400 405 410	
ccc gca gtc tat gaa gtc atg aag aac tgc tgg cac ctg gac gcc gcc	1417
Pro Ala Val Tyr Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala	
415 420 425	

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atg cgg ccc tcc ttc cta cag ctc cga gag cag ctt gag cac atc aaa 1465
 Met Arg Pro Ser Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys
 430 435 440

acc cac gag ctg cac ctg tgacggctgg cctccgcctg ggtcatgggc 1513
 Thr His Glu Leu His Leu
 445 450

ctgtggggac tgaacctgga agatcatgga cctggtgccc ctgctcactg ggcccagagcc 1573
 tgaactgagc cccagcgggc tggcgggcct ttttcctgcg tcccagcctg caccctccg 1633
 gcccctctc tcttggaacc acctgtggg cctggggagc ccaactgaggg gccagggagg 1693
 aaggaggcca cggagcggga ggcagcggc caccacgtcg ggcttccctg gcctcccgcc 1753
 actgccttc ttagagtttt attcctttcc ttttttgaga tttttttcc gtgtgtttat 1813
 tttttattat ttttcaagat aaggagaaaag aaagtaccca gcaaatgggc attttacaag 1873
 aagtacgaat cttatttttc ctgtcctgcc cgtgaggggtg ggggggaccg ggcccctctc 1933
 tagggacccc tcgccccagc ctcatctccc attctgtgtc ccatgtcccg tgtctcctcg 1993
 gtcgccccgt gtttgcgctt gaccatgttg cactgtttgc atgcgcccga ggcagacgtc 2053
 tgtcaggggc ttggatttcg tgtgccgctg ccaccgcgcc accgccttg tgagatggaa 2113
 ttgtaataaa ccacgccatg aggacaccgc cgccgcctc ggcgcttctt ccaccgaaaa 2173
 aaaaaaaaaa aaaa 2187

<210> 5
 <211> 450
 <212> PRT
 <213> Homo sapiens

<400> 5
 Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr Glu Cys Ile Ala
 1 5 10 15
 Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu Pro Phe Cys Lys
 20 25 30
 Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
 35 40 45
 Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
 50 55 60
 Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
 65 70 75 80

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Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
 85 90 95
 Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
 100 105 110
 Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
 115 120 125
 Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
 130 135 140
 Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
 145 150 155 160
 Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
 165 170 175
 Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
 180 185 190
 Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
 195 200 205
 Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
 210 215 220
 Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
 225 230 235 240
 Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
 245 250 255
 Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
 260 265 270
 Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
 275 280 285
 Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
 290 295 300
 Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
 305 310 315 320
 Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
 325 330 335
 Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp
 340 345 350
 Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp
 355 360 365
 Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg
 370 375 380

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Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu
 385 390 395 400

Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr
 405 410 415

Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser
 420 425 430

Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu
 435 440 445

His Leu
 450

<210> 6

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:9E10-myc
 epitope tag

<400> 6

Val Asp Met Glu Gln Lys Leu Ile Ala Glu Glu Asp Leu Asn
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